

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: French et al.

Serial No.: 09/497,822

Examiner: M. Pak Group Art Unit: 1646

Filed: February 3, 2000

ANDROGEN RECEPTOR PROTEINS, RECOMBINANT DNA MOLECULES

CODING FOR SUCH, AND USE OF SUCH COMPOSITIONS

RECEIVED

Date: July 31, 2001

BOX SEQUENCE Commissioner for Patents Washington, DC 20231

TECH CENTER 1600/2900

STATEMENT IN SUPPORT OF FILING A **SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

Sir:

For:

I hereby state that the content of the paper and computer readable copies of the Sequence listing, submitted concurrently herewith in accordance with 37 CFR § 1.821(c) and (e), are the same. I also hereby state as required by 37 CFR § 1.821(h) that the paper and computer readable copies contain no new matter, nor do they go beyond the disclosure of the application as filed.

Respectfully submitted,

Karen A. Magri

Registration No. 41,965

Customer Number:

20792 PATENT TRADEMARK OFFICE

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner For Patents, Washington, DC 20231, on July 31, 2001.

Traci A. Brown

Date of Signature: July 31, 2001

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AHG U 7 2001

O COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

g 1003011(3).
1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
7. Other:
Applicant Must Provide:
An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).
For questions regarding compliance to these requirements, please contact:
· or region likelihi eration call (/U3/ 308 4046
FOLCE Submission Help call (703) 308 4343
For Patentin software help, call (703) 308-6856
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SEQUENCE LISTING

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DIIG U 7 2001

TECH CENTER 1600/2900

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Wilson, Elizabeth

Joseph, David

Lubahn, Dennis

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Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp 85 90 95

Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu 100 110

Asp Glu Glu Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His 115 120 125

Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser 130 135 140

Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser 145 150 155 160

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Pro Leu Cly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro 275 280 285

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Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu 435 440 445

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Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn 630 635 640

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Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu 690 700 Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val 705 710 715 720

Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp 735

Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala 740 745 750

Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe 755 760 765

Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met 770 780

Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp 785 790 795 800

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Glu Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile 35 40 45

Ala Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg 50 60

Arg Arg Arg Gln Gln His Pro Glu Asp Gly Ser Pro Gln Ala His 70 75 80

Ile Arg Gly Thr Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro 85 90 95

Ser Gln Gln Gln Ser Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu 100 105 110

Pro Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln 115 120 125

Pro Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu 130 140 Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp 150 155 160

Ile Lys Asp Ile Leu Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln 175

Gln Gln Gln Glu Val Ile Ser Glu Gly Ser Ser Ser Val Arg Ala 195 200 205

Arg Glu Ala Thr Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly
210 220

Gly Asn Ser Thr Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val 230 235 240

Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro 245 250 255

Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly 260 265 270

Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys 275 280 285

Gly Leu Ser Leu Asp Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala 290 295 300

Glu Tyr Ser Ser Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu 305 310 310 320

Ser Leu Gly Cys Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu 325 330 335

Glu Ile Pro Ser Ser Leu Ser Leu Tyr Lys Ser Gly Ala Val Asp Glu 345 350

Ala Ala Ala Tyr Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu 355 360 365

Ser Gly Pro Pro His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile 370 375 380

Lys Leu Glu Asn Pro Ser Asp Tyr Gly Ser Ala Trp Ala Ala Ala 385 390 395 400 Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Gly Ser Val 405 410 415

Ala Gly Pro Ser Thr Gly Ser Pro Pro Ala Thr Ala Ser Ser Trp
420
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His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly 435 440 445

Gly Gly Gly Ser Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr 450 460

Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Ser Gln Glu Gly Asp Phe 475 480

Ser Ala Ser Glu Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro 485 490 495

Tyr Pro Ser Pro Ser Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu 500 510

Asn Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp 515 520 525

His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu 530 540

Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys
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560

Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys 565 570 575

Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg 580 590

Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met 595 600 605

Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln 610 620

Glu Glu Gly Glu Asn Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser 630 635 640

Gln Lys Met Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile 645 650

Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly

His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu 675 680 685

Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys 690 695

Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val 705 710 715 720

Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg 725 730 735

Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu 740 745 750

Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys 755 760 765

val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr 770 780

Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Phe Ser Ile Ile 785 790 800

Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met 805 810 815

Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn 820 830

Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp 835

Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu 850 860

Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala 865 870 880

Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Ser 885 890 895

Pro Cys Ile Ser Thr His Ser Glu Asp Leu Glu Pro Asn Thr Gln Thr 900 905 910

His Leu Phe Pro Phe Gln Met Ser Ser Ala Cys Tyr Ile Thr Leu His 915 920 925 Tyr Phe Ser Gly Met Gly Leu Gly Gly Asn Ser Ser Thr Asp Val Gln 930 940

Ser Val Met Asn Met Phe Pro Lys Phe Tyr Phe Leu Gly Phe Ser Phe 945 955 960

Phe Leu Phe Leu Leu Cys Leu Phe Tyr Pro Pro Met Ala His Phe 965 970 975

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